Table S1: Biochemical properties of *in vitro* Dps binding to linear DNA sequences containing the promotor sequences *recA* (252 bp), *flu*P (401 bp), λ P_R (483 bp), and *rrnB* P1 (120 bp). Mean apparent K_D and mean Hill coefficients were calculated based on the analysis of gel-shift assays performed for each DNA template. Related to **Figure 3**.

Template	**Mean apparent K_D ± SEM [μM]**	**Mean Hill Coef. ± SEM**
recA	0.54 ± 0.06	3.33 ± 0.31
rrnB P1	0.57 ± 0.04	2.97 ± 0.17
flu	0.64 ± 0.03	3.10 ± 0.11
λ P_R	0.77 ± 0.04	3.29 ± 0.18

Table S2: Statistics of single-molecule transcription experiments. Denoted are the number of traces, dwell times measured, average elongation rates, and pause probabilities (SP = short pause lengths between 1 - 5 s; LP = long pause lengths between 5 – 100 s), respectively, for each type of single-molecule transcription experiment. Related to **Figure 5**.

	AF	**AF + Dps**	**OF**	**OF + Dps**
N	*76*	*47*	*49*	*38*
Dwell times	12,839	7,341	5,687	4,339
Elongation rate [nt/s]	26.6 ± 0.3	26.3 ± 0.4	23.5 ± 0.3	22.7 ± 0.5
SP probability	0.36 ± 0.006	0.37 ± 0.008	0.44 ± 0.01	0.43 ± 0.01
LP probability	0.024 ± 0.003	0.025 ± 0.003	0.038 ± 0.005	0.029 ± 0.005

Table S3: Primer sequences used for the production of DNA tether constructs. Related to STAR Methods section.

Oligonucleotide	Sequence
1	5'- GACCGAGATAGGGTTGAGTG
2	5'- CCATCTTGGTCTCCCCTACGCTCTAGAACTAGTGGATCCCCC
3	5'- CCATCTTGGTCTCCTAGGCGTCAGCCTGCGAAGCAGTGGC
4	5'- CCATCTTGGTCTCCTGTCAACACCACTTTGCTCCGAGGTT
5	5'- CCATCTTGGTCTCCGACAGCGCCATTCGCCATTCAGGCTG
6	5'- CTTCTGCTTTCCTGATGCAAAAAC
7	5'- CTGCGGTCTCGCCCGACCGGCTCCAGATTTATCAGC
8	5'- CTGCGGTCTCGTCAAAAACTGGAACAACACTCAACCC
9	5'- CTGCGGTCTCGTAGGAGGCGCCATTCGCCATTCAGG
10	5'- CTGCGGTCTCGCCGGGTTGCAGCACTGGGGCCAGATG
11	5'- GACCGAGATAGGGTTGAGTG
12	5'- CAGGGTCGGAACAGGAGAGC
13	5'- CTGCGGTCTCGCCCGACCGGCTCCAGATTTATCAGC
14	5'- CTGCGGTCTCGTCAATTACGCGCAGCGTGACCGCTAC
15	5'- CTGCGGTCTCGTAGGCCGATTTAGAGCTTGACGGGG
16	5'- CTGCGGTCTCGCGGGTTGCAGCACTGGGGCCAGATG

Table S4: Primer sequences used for the production of DNA promoter templates. Related to STAR Methods section.

Oligonucleotide	Sequence
rrnB P1 pIA536	5'- TCAGGAATTCGAACGCGGTCAGAAAATTATTTT
rrnB P1 pIA536	5'- GTTCGGCATGGGGTCAGGTG
λ P_R pIA1240	5'- CGTTAAATCTATCACCGCAAGG
λ P_R pIA1240	5'- CAGTTCCCTACTCTCGCATG
recA pIA1222	5'- GTAAAACGACGGCCAGT
recA pIA1222	5'- ATTACGAATTCGCGAGAGACATCG
P*flu E. coli* genomic DNA	5'- ATTTTCTTCTGAACCTGTCGTG
P*flu E. coli* genomic DNA	5'- ACGAAAGCGCCCGTCATGTG